

O I P E

JUL 29 2002

SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> IMHOF, BEAT ALBET  
AURRAND-LIONS, MICHEL

<120> VASCULAR ADHESION MOLECULES AND MODULATION OF THEIR  
FUNCTION

<130> 11422/0264679

<140> 09/524,531

<141> 2000-03-13

<150> EP 99.200746.8

<151> 1999-03-11

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> modified\_base

<222> (6)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (10)..(12)

<223> a, t, c, g, other or unknown

<400> 1

tayagntgyn nngcytcyaa

20

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> modified\_base

<222> (10)..(12)

<223> a, t, c, g, other or unknown

<400> 2

taycrgtgyn nngcytcyaa

20

<210> 3

<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<220>  
<221> modified\_base  
<222> (10)..(12)  
<223> a, t, c, g, other or unknown

<400> 3  
taytaytgyn nngcytcyaa

20

<210> 4  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 4  
gaggtacttg catgtgct

18

<210> 5  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 5  
cgacaggtgt cagataaca

19

<210> 6  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 6  
caccctcctc actcgt

16

<210> 7  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer used  
for detection of JAM-2 transcript

<400> 7

gactcacaga caagtgac

18

<210> 8

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer used  
for detection JAM-2 transcript

<400> 8

caccctcctc actcgt

16

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for  
Hprt cDNA

<400> 9

gttgataca ggccagactt tgttg

25

<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for  
Hprt cDNA

<400> 10

gagggtaggc tggcctatag gct

23

<210> 11

<211> 1943

<212> DNA

<213> Mus musculus

<400> 11

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aatccagcaa ccgaaaccca gtggtacatg aatttgaaag tgtggaattg tcttgcacat 180  
ttacggactc acagacaagt gaccctagga ttgaatggaa gaaaatccaa gatggccaaa 240  
ccacatatgt gtattttgac aacaagattc aaggagacct ggcaggctcg acagatgtgt 300  
ttggaaaaaac ttccctgagg atctggaatg tgacacgatc ggattcagcc atctatcgct 360  
gtgaggtcgt tgctctaaat gaccgaaaag aagttgatga gattaccatt gagttaattg 420  
tgcaagtga ggcagtggacc cctgtctgca gaattccagc cgctgtacct gtaggcaaga 480  
cggcaacact gcagtggcaa gagagcgagg gctatccccg gcctcactac agctgggtacc 540  
gcaatgatgt gccactgcct acagattcca gagccaatcc caggttccag aattcctctt 600  
tccatgtgaa ctcgagagaca ggcactctgg ttttcaatgc tgtccacaag gacgactctg 660  
ggcagtacta ctgcattgct tccaatgacg cagggtgcagc cagggtgtgag gggcaggaca 720  
tggaagtcta tgatttgaac attgctggga ttattggggg agtccttgtt gtccttattg 780

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gtaaacaaga	tggagaaagc	tataagagcc	caggggaagca	tgacgggtgt	aactacatcc	900
ggacgagtga	ggaggggtgac	ttcagacaca	aatcgctcctt	tgttatctga	cacctgtcgg	960
ctgggagagc	acatgcaagt	acctctgttg	gaagctggtc	acagggctgc	tgtgagccca	1020
gagctcctga	caaagccacc	cgggcagaag	ctttttgttt	tggccaaagt	tgatgactcc	1080
ttccttcctt	ccttcctcct	taacaagcca	caagaataaa	aggaagcctc	ctgaagatgg	1140
atgtagacac	agattgtttg	tagcctgacc	tcattatggg	gattaggggtg	atcttcaagg	1200
cctttctggg	ctccgttctc	ccatgcaggg	caatttggac	tgtttttgcc	ccaggctgtt	1260
tagctgccag	gacaacactg	gcagagagag	gctgaggcgc	tgggctgcag	tagcagcagg	1320
caacagcctg	atgcctgtga	cagtgcacca	ggaagggtttt	caggcagtg	cttgctccct	1380
ggaccctgac	ccaccgtgtt	gcctctgttg	attggccagt	actgtcattt	ccatcctgga	1440
gaatgtgttt	ggaatcagca	ttttataaaa	aaccacaatc	agaaaggtga	aattgcttgc	1500
tgggaagagg	gctctgaccc	aggaaactct	ccttcccaag	agatgccagg	agataggaga	1560
acctgtctgt	cttaagtctg	aaatgggtact	gaagtctcct	tttctattgg	tcttgcttat	1620
tttataaaaa	tttaacattc	taaattttgc	tagagatgta	ttttgattac	tgaaaatttc	1680
tatataaact	gtaaataat	tgccatacag	tgtttcaaaa	cgtatttttt	tataatgagt	1740
tcaacttaag	gtagaaggct	tgggctgcta	gtgtttaatt	ggaaaatacc	agtagtaaag	1800
tcttttaagg	agttttctta	aggaggctgg	ctgaatatct	ctttgttcaa	aagaagtttt	1860
agcatttttc	ataagaaaa	ttactctgtc	tgaccactgt	tgcttaggaa	accattaaag	1920
aattccaatc	taaaaaaaaa	aaa				1943

<210> 12  
 <211> 1631  
 <212> DNA  
 <213> Mus musculus

E,

<400> 12	
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agagctaata	tctgcccga
ccctcccttc	aacctctctc
ggccagaaga	cctgccccca
tcgggacagg	acccgcccct
ggcgaagtgc	tgggagaccc
cagccagctg	gcgcccgcgt
gctacactac	ttgatcgctg
agaccaccgt	caagaagtca
cccaaagaag	actacctcct
ggtctactac	caacaggctc
caatatacga	atcaaaaatg
cgctccgact	gagcaaggcc
ggctcctgct	gttccctgct
gctacgatgc	caggataaag
cacaagtttg	ctaggggaatc
acacgaatct	ggaattctgc
ctgcgaagcc	cggaaactctg
tgttctcaac	ataagcggca
atgtggcctt	ggcacatgct
ccagaagggc	agtcctgcat
aaaatccttt	ataatttaaa
gttattaaaa	tattgtaaaa
aggggagttc	atcagaagtt
ttcttgccat	cactaaatta
aatattctgg	tttttgaagg
tgtaaggcta	atccaagaag
aaaaaaaaatt	c

<210> 13  
 <211> 310  
 <212> PRT

<213> Mus musculus

<400> 13

Met Ala Leu Ser Arg Arg Leu Arg Leu Arg Leu Tyr Ala Arg Leu Pro  
1 5 10 15  
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Asn Leu Lys Ser Ser Asn Arg Asn Pro Val Val His Glu Phe Glu Ser  
35 40 45  
Val Glu Leu Ser Cys Ile Ile Thr His Ser Gln Thr Ser Asp Pro Arg  
50 55 60  
Ile Glu Trp Lys Lys Ile Gln Asp Gly Gln Thr Thr Tyr Val Tyr Phe  
65 70 75 80  
Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly Arg Thr Asp Val Phe Gly  
85 90 95  
Lys Thr Ser Leu Arg Ile Trp Asn Val Thr Arg Ser Asp Ser Ala Ile  
100 105 110  
Tyr Arg Cys Glu Val Val Ala Leu Asn Asp Arg Lys Glu Val Asp Glu  
115 120 125  
Ile Thr Ile Glu Leu Ile Val Gln Val Lys Pro Val Thr Pro Val Cys  
130 135 140  
Arg Ile Pro Ala Ala Val Pro Val Gly Lys Thr Ala Thr Leu Gln Cys  
145 150 155 160  
Gln Glu Ser Glu Gly Tyr Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn  
165 170 175  
Asp Val Pro Leu Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Gln Asn  
180 185 190  
Ser Ser Phe His Val Asn Ser Glu Thr Gly Thr Leu Val Phe Asn Ala  
195 200 205  
Val His Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp  
210 215 220  
Ala Gly Ala Ala Arg Cys Glu Gly Gln Asp Met Glu Val Tyr Asp Leu  
225 230 235 240  
Asn Ile Ala Gly Ile Ile Gly Gly Val Leu Val Val Leu Ile Val Leu  
245 250 255  
Ala Val Ile Thr Met Gly Ile Cys Cys Ala Tyr Arg Arg Gly Cys Phe  
260 265 270  
Ile Ser Ser Lys Gln Asp Gly Glu Ser Tyr Lys Ser Pro Gly Lys His  
275 280 285  
Asp Gly Val Asn Tyr Ile Arg Thr Ser Glu Glu Gly Asp Phe Arg His  
290 295 300  
Lys Ser Ser Phe Val Ile

305

310

<210> 14  
 <211> 298  
 <212> PRT  
 <213> Mus musculus

<400> 14

Met Ala Arg Ser Pro Gln Gly Leu Leu Met Leu Leu Leu Leu His Tyr  
 1 5 10 15

Leu Ile Val Ala Leu Asp Tyr His Lys Ala Asn Gly Phe Ser Ala Ser  
 20 25 30

Lys Asp His Arg Gln Glu Val Thr Val Ile Glu Phe Gln Glu Ala Ile  
 35 40 45

Leu Ala Cys Lys Thr Pro Lys Lys Thr Thr Ser Ser Arg Leu Glu Trp  
 50 55 60

Lys Lys Val Gly Gln Gly Val Ser Leu Val Tyr Tyr Gln Gln Ala Leu  
 65 70 75 80

Gln Gly Asp Phe Lys Asp Arg Ala Glu Met Ile Asp Phe Asn Ile Arg  
 85 90 95

Ile Lys Asn Val Thr Arg Ser Asp Ala Gly Glu Tyr Arg Cys Glu Val  
 100 105 110

Ser Ala Pro Thr Glu Gln Gly Gln Asn Leu Gln Glu Asp Lys Val Met  
 115 120 125

Leu Glu Val Leu Val Ala Pro Ala Val Pro Ala Cys Glu Val Pro Thr  
 130 135 140

Ser Val Met Thr Gly Ser Val Val Glu Leu Arg Cys Gln Asp Lys Glu  
 145 150 155 160

Gly Asn Pro Ala Pro Glu Tyr Ile Trp Phe Lys Asp Gly Thr Ser Leu  
 165 170 175

Leu Gly Asn Pro Lys Gly Gly Thr His Asn Asn Ser Ser Tyr Thr Asn  
 180 185 190

Glu His Glu Ser Gly Ile Leu Gln Phe Asn Met Ile Ser Lys Met Asp  
 195 200 205

Ser Gly Glu Tyr Tyr Cys Glu Ala Arg Asn Ser Val Gly His Arg Arg  
 210 215 220

Cys Pro Gly Lys Arg Met Gln Val Asp Val Leu Asn Ile Ser Gly Ile  
 225 230 235 240

Ile Ala Thr Val Val Val Val Ala Phe Val Ile Ser Val Cys Gly Leu  
 245 250 255

Gly Thr Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
 260 265 270

Phe Gln Lys Gly Ser Pro Ala Ser Lys Val Thr Thr Met Gly Glu Asn  
 275 280 285

Asp Phe Arg His Thr Lys Ser Phe Ile Ile  
 290 295

<210> 15  
 <211> 310  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 Met Ala Leu Arg Arg Pro Pro Arg Leu Arg Leu Cys Ala Arg Leu Pro  
 1 5 10 15

Asp Phe Phe Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly Ala Val  
 20 25 30

Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu Phe Glu Ser  
 35 40 45

Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr Ser Asp Pro Arg  
 50 55 60

Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr Thr Tyr Val Phe Phe  
 65 70 75 80

Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly Arg Ala Glu Ile Leu Gly  
 85 90 95

Lys Thr Ser Leu Lys Ile Trp Asn Val Thr Arg Arg Asp Ser Ala Leu  
 100 105 110

Tyr Arg Cys Glu Val Val Ala Arg Asn Asp Arg Lys Glu Ile Asp Glu  
 115 120 125

Ile Val Ile Glu Leu Thr Val Gln Val Lys Pro Val Thr Pro Val Cys  
 130 135 140

Arg Val Pro Lys Ala Val Pro Val Gly Lys Met Ala Thr Leu His Cys  
 145 150 155 160

Gln Glu Ser Glu Gly His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn  
 165 170 175

Asp Val Pro Leu Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn  
 180 185 190

Ser Ser Phe His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala  
 195 200 205

Val His Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp  
 210 215 220

Ala Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu  
 225 230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val Leu  
 245 250 255

Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly Tyr Phe  
 260 265 270  
 Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro Gly Lys Pro  
 275 280 285  
 Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly Asp Phe Arg His  
 290 295 300  
 Lys Ser Ser Phe Val Ile  
 305 310

<210> 16  
 <211> 212  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile Lys Asn Val Thr Arg  
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 20 25 30  
 Gly Gln Asn Leu Glu Asp Thr Val Thr Leu Glu Val Leu Val Ala Pro  
 35 40 45  
 Ala Val Pro Ser Cys Glu Val Pro Ser Ser Ala Leu Ser Gly Thr Val  
 50 55 60  
 Val Glu Leu Arg Cys Gln Asp Lys Glu Gly Asn Pro Ala Pro Glu Tyr  
 65 70 75 80  
 Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu Glu Asn Pro Arg Leu Gly  
 85 90 95  
 Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met Asn Thr Lys Thr Gly Thr  
 100 105 110  
 Leu Gln Phe Asn Thr Val Ser Lys Leu Asp Thr Gly Glu Tyr Ser Cys  
 115 120 125  
 Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg Cys Pro Gly Lys Arg Met  
 130 135 140  
 Gln Val Asp Asp Leu Asn Ile Ser Gly Ile Ile Ala Ala Val Val Val  
 145 150 155 160  
 Val Ala Leu Val Ile Ser Val Cys Gly Leu Gly Val Cys Tyr Ala Gln  
 165 170 175  
 Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser Phe Gln Lys Ser Asn Ser  
 180 185 190  
 Ser Ser Lys Ala Thr Thr Met Ser Glu Asn Asp Phe Lys His Thr Lys  
 195 200 205  
 Ser Phe Ile Ile



210

<210> 17  
<211> 1296  
<212> DNA  
<213> Homo sapiens

<400> 17  
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ccagtgggtac aggaatttga aagtgtggaa ctgtcttgca tcattacgga ttcgcagaca 180  
agtgacccca ggatcgagtg gaagaaaatt caagatgaac aaaccacata tgtgtttttt 240  
gacaacaaaa ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 300  
aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt cgttgctcga 360  
aatgaccgca aggaaattga tgagattgtg atcgagttaa ctgtgcaagt gaagccagtg 420  
acccctgtct gtagagtgcc gaaggctgta ccagtaggca agatggcaac actgcactgc 480  
caggagagtg agggccaccc cgggcctcac tacagctggg atcgcaatga tgtaccactg 540  
cccacggatt ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 600  
acaggcactt tgggtgtcac tgctgttcac aaggacgact ctgggcagta ctactgcatt 660  
gcttccaatg acgcaggctc agccagggtg gaggagcagg agatggaagt ctatgacctg 720  
aacattggcg gaattattgg ggggggtctg gttgtccttg ctgtactggc cctgatcacg 780  
ttgggcatct gctgtgcata cagacgtggc tacttcatca acaataaaca ggatggagaa 840  
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gacttcagac acaagtcac gtttgtgatc tgagaccggt gtgtggctga gagcgcacag 960  
agccgcacgt gcacatacct ctgctagaaa ctctgtcaa ggcagcgaga gctgatgcac 1020  
tcgacagagc tagacactct tcaaagcttt tcgtttggca aggtgaccac tactctttta 1080  
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aaccaaactg ggtgcgttca ctgaggtggg gtccttaatt tgtttttggc ctgattccca 1200  
tgaaaataag gggcttttaa gagtttggtg cgtaaaaccc cccgcttggg ccttggaaac 1260  
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E,  
<210> 18  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: sequence  
surrounding C-terminal cysteine of C2 domain  
(endothelial cell line t-end)

<220>  
<221> MOD\_RES  
<222> (4)  
<223> Any amino acid

<400> 18  
Tyr Arg Cys Xaa Ala Ser  
1 5

<210> 19  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: sequence

surrounding the C-terminal cysteine of C2 domain  
(endothelial cell line t-end)

<220>  
<221> MOD\_RES  
<222> (4)  
<223> Any amino acid

<400> 19  
Tyr Gln Cys Xaa Ala Ser  
1 5

<210> 20  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: sequence  
surrounding the C-terminal cysteine of C2 domain  
(endothelial cell line t-end)

<220>  
<221> MOD\_RES  
<222> (4)  
<223> Any amino acid

<400> 20  
Tyr Tyr Cys Xaa Ala Ser  
1 5

<210> 21  
<211> 300  
<212> PRT  
<213> Mus musculus

<400> 21  
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Ala Gln Ser Asp Val Gln Val Pro Glu Met Glu Ser Ile Lys Leu Thr  
35 40 45  
Cys Thr Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Val  
50 55 60  
Gln Gly Ser Thr Thr Ala Leu Val Cys Tyr Asn Ser Gln Ile Thr Ala  
65 70 75 80  
Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser Glu Gly Ile Thr Phe Ser  
85 90 95  
Ser Val Thr Arg Lys Asp Asn Gly Glu Tyr Thr Cys Met Val Ser Glu  
100 105 110  
Glu Gly Gly Gln Asn Tyr Gly Glu Val Ser Ile His Leu Thr Val Leu

115					120					125						
Val	Pro	Pro	Ser	Lys	Pro	Thr	Ile	Ser	Val	Pro	Ser	Ser	Val	Thr	Ile	
130					135					140						
Gly	Asn	Arg	Ala	Val	Leu	Thr	Cys	Ser	Glu	His	Asp	Gly	Ser	Pro	Pro	
145					150					155					160	
Ser	Glu	Tyr	Ser	Trp	Phe	Lys	Asp	Gly	Ile	Ser	Met	Leu	Thr	Ala	Asp	
165					170					175						
Ala	Lys	Lys	Thr	Arg	Ala	Phe	His	Asn	Ser	Ser	Phe	Thr	Ile	Asp	Pro	
180					185					190						
Lys	Ser	Gly	Asp	Leu	Tyr	Phe	Asp	Phe	Val	Thr	Ala	Phe	Asp	Ser	Gly	
195					200					205						
Glu	Tyr	Tyr	Cys	Gln	Ala	Gln	Asn	Gly	Tyr	Gly	Thr	Ala	Met	Arg	Ser	
210					215					220						
Glu	Ala	Ala	His	Met	Asp	Ala	Val	Glu	Leu	Asn	Val	Gly	Gly	Ile	Val	
225					230					235					240	
Ala	Ala	Val	Leu	Val	Thr	Leu	Ile	Leu	Leu	Gly	Leu	Leu	Ile	Phe	Gly	
245					250					255						
Val	Trp	Phe	Ala	Tyr	Ser	Arg	Gly	Tyr	Phe	Glu	Thr	Thr	Lys	Lys	Gly	
260					265					270						
Thr	Ala	Pro	Gly	Lys	Lys	Val	Ile	Tyr	Ser	Gln	Pro	Ser	Thr	Arg	Ser	
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<210> 22  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: sequence  
 surrounding the C-terminal cysteine of C2 domain  
 (endothelial cell line t-end)

<220>  
 <221> MOD\_RES  
 <222> (2)  
 <223> Arg, Gln, Tyr, Ser

<220>  
 <221> MOD\_RES  
 <222> (4)  
 <223> Any amino acid

<220>  
 <221> MOD\_RES  
 <222> (8)  
 <223> Any amino acid

<400> 22

Tyr Xaa Cys Xaa Ala Ser Asn Xaa Gly .  
1 5

E,  
concl'd